

OM of: US-08-711-417c-165 to: A_Geneseq_032802:* out_format : pfs

Date: Aug 28, 2002 10:05 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame_n2p.model -DEV=xlp
-Q=/cygn2/USPRO-spool/6228611/runat_28082002_100210_13550/app_query.fasta_1.1639
-DB=A_Geneseq_032802 -QFMT=fastan -SUFFIX=rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
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-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=6228611@cgnl_1.164 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-711-417c-165
Query length: 1551
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 11107396
Search time (sec): 119.550000

score.list:

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW70971

seq_documentation_block:

ID AAW70971 standard; Protein; 516 AA.

AC AAW70971;

DT 11-JAN-1999 (first entry)

XX Human Ikaro isoform h1k-1.

DE Ikaro: h1k-1; transcription factor; human; lymphocyte;

KW cell differentiation; T cell; cancer; immunodeficiency;

KW Alzheimer's disease; therapy; diagnosis.

XX Homo sapiens.

XX Location/Qualifiers

Key 119..139

Region /note= "zinc finger motif"

Region 147..167

Region /note= "zinc finger motif"

Region 175..195

Region /note= "zinc finger motif"

Region 203..224

Region /note= "zinc finger motif"

Region 461..481

Region /note= "zinc finger motif"

Region 489..511

Region /note= "zinc finger motif"

CA2194256-A.

05-MAR-1998.

02-JAN-1997; 97CA-2194256.

05-SEP-1996; 96US-0711417.

(GEO) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1998-378292/33.

N-PSDB; AAV42840.

New nucleic acid encoding Ikaro protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation

Claim 1; Page 127-129; 158pp; English.

This is the amino acid sequence of human Ikaro protein isoform h1k-1, deduced from a cDNA clone (see AAV42840) obtained from a Jurkat T cell line cDNA library. Native Ikaro is active in the early stages of lymphocyte differentiation, binding to and activating the CD3-delta gene enhancer (see AAV42804). Proteins of the human Ikaro family (see also AAV70964 and AAV70969) are isoforms that arise from differential splicing of Ikaro gene transcripts, and contain different combinations of zinc fingers. They are expressed primarily in T cells in the adult and may play a role as a genetic switch regulating entry into the T cell lineage. The human and murine sequences (see also AAV70963 and AAV70965-68) are very similar. The invention provides Ikaro nucleic acids, vectors and host cells expressing Ikaro polypeptides. These can be used to treat T and B cell diseases (e.g. immune deficiencies caused by

CC drugs, radiation or cancer), to control expression of heterologous
CC genes placed under control of an Ikaro's-responsive element, to
CC treat nervous system diseases (e.g. Alzheimer's disease) and to
CC modulate cell division, amplification or differentiation, especially
CC in haematopoietic cells. Some Ikaro's isoforms are antagonistic of
CC others and may be used to inhibit interaction with DNA sequences.
XX
SQ

Sequence 516 AA;

alignment_scores:

Quality: 2750.00 Length: 516
Ratio: 5.329 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-711-417c-165 x AAW70971 ..

Align seg 1/1 to: AAW70971 from: 1 to: 516

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101  CCGAGGACCTCTCCACCACTCCGGGAGGACAGCAAGCTCCAGAGGTGAC 150
34  roGluAspLeuSerThrThrSerGlyGlyGlnGlnSerSerLysSerAsp 50
151  AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
51  ArgValValAlaSerAsnValLysValGluThrGlnSerAspGluGluA 67
201  TGGGCGTGGCTGTGAATGAATGGGGAAGAATGTCGGGAGATTACGAA 250
67  nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArg 84
251  TGCTTCATGCTCGGAGAGAAATCAATGGCTCCACAGGGGACCAAGGC 300
84  etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301  AGCTCGGCTTTGTGGAGTGTGGAGCATTCGACTTCCTTAACGGAAACT 350
101  SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351  AAGTGTGATATCTGTGGATCATTTTGCATCGGGCCCAATGTGCTCATGG 400
117  uLysCysAspIleCysGlyIleIleCysIleGlyProAsnValLeuMetv 134
401  TTCACAAAAGAACCCACTGGAGAACGCCCTTCCAGTGCAATCAGTGC 450
134  alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
451  GGGGCTCATTTACCCAGAGGCAACCTGCTCCGGCCACATCAAGTGCA 500
151  GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501  TTCGGGGAGAACCCCTTCAATGCCACCTCTGCAACTAGCGCTGCCGCC 550
167  sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 184
551  GGAGGAGCCCTCTACTGGCCACTCAGGAGCGCACTCCGTTGGTAAACCT 600
184  rArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
601  CACAAATGTGGATATTGTGGCCGAAGCTATAAAGCGAAGCTCTTTAGA 650
201  HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgThrSerLeuGl 217
651  GGNACATAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCGCTCCGG 700
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||||| 751 GAAGACCTGTGCAAGATAGATGATCAGAGATCTCTCGTCTGGACAGACT 800
||||| 251 GluAspLeuCysLysIleGlySerGluArgSerLeuValLeuAspArgLe 267
||||| 801 AGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
||||| 267 uAlaSerAsnValAlaLysArgLysSerMetProGlnLysPheLeuG 284
||||| 851 GGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCACAGTGCACGAGAAG 900
||||| 284 lyAspLysGlyLeuSerAspThrProTyrAspSerAlaThrTyrGluLys 300
||||| 901 GAGACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACACGC 950
||||| 301 GluAsnGluMetMetLysSerHisValMetAspGlnAlaIleAsnAsnAl 317
||||| 951 CATCAACTACTGGGGCGGAGTCCCTGCGCGCGCTGGTGCAGACGCCCC 1000
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||||| 1401 CTTCTCTGATCAGTCTCATGTACACCATCCACATGGGCTGCCACGGCTTC 1450
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seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT: AAB42333

seq_documentation_block:

ID AAB42333 standard; Protein: 519 AA.

AC AAB42333;

XX DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF2097 polypeptide sequence SEQ ID NO:4194.

XX KW Human: open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX PN W0200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX DR WPI; 2000-602362/57.

XX DR N-PSDB; AAC76542.

XX PT Novel nucleic acids and peptides derived from open reading frame X,
 XX useful for treating e.g. cancers, proliferative disorders,
 XX neurodegenerative disorders and cardiovascular disease.

XX PS Claim 11; Page 3390-3391; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 519 AA;

alignment_scores:
 Quality: 2644.50 Length: 519
 Ratio: 5.175 Gaps: 3
 Percent Similarity: 98.459 Percent Identity: 96.724

alignment_block:
 US-08-711-417c-165 x AAB42333 ..
 Align seg 1/1 to: AAB42333 from: 1 to: 519

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 51 CCCCCCTTAAGCGATACCTCCAGATGAGGGGAGGAGCCCATGCCATCC 100
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 17 rProProValSerAspThrProAspGluGlyAspGluProMetProIleP 34
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 101 CGGAGGACCTCTCCACCACCTCGGGAGGAGCAAAAGCTCCAAGAGTGAC 150
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 34 roGluAspLeuSerThrThrSerGlyGlyGlnGlnSerSerLysSerAsp 50
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 151 AGAGTCGTGGCCAGTAAATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAA 200
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 51 ArgValValAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
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 201 TGGCGGTGCTGTGAATGAGTGGGAAGAAATGTGCGGAGGATTTACGAA 250
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 67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
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 401 TTCACAAAAGAGCCACACTGGAGAACCGCCCTCCAGTGAATCAGTGC 450
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 134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
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 501 TTCGGGGAGAGCCCTTCAATGCCACTCTGCAACTAGCCTGCGCGCC 550
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 167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArg 184
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 184 rGArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
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 601 CACAAATGTGGATATTGTGGCCGAAGCTATAAAGCAGGAGCAAGCTTTAGA 650
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 201 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 217
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 651 GGAACATAAGAGCGCTGCCACAACTACTTTGGAAGCATGGGCTTCCGG 700
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 217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
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 701 GCACACTGTCCAGTCAATTAAGAGAACTAAGCAGACAGTGAATGGCA 750
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 234 LyThrLeuTyrProValLysGluGluThrAsnHisSerGluMetAla 250
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 751 GAAGACCTGTGCAAGATAGATGATCAGAGATCTCTCGTCTGGACAGACT 800

us-08-711-417c-165.rag

Wed Aug 28 10:05:31 2002

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251 GluAspLeuGlySerGluArgSerLeuValLeuAspArgLe 267
801 AGCAAGTAATGCGCAACAGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
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267 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 284
851 GGGACAAAGGCGCTGCGGACAGCCCTACGAC...AGTCCACAGTACGAG 897
284 LysPlyGlyLeuSerAspThrProTyrAspSerSerAlaSerTyrGlu 300
898 AAGGAGACCAATATGATGAAGTCCACGTGATGGACCAAGCCATCAACA 947
301 LysGluAsnGluMetMetLysSerHisValMetAspGlnAlaIleAsnAs 317
948 CGGCATCAACTACTGCGGGCGCGAGTCCCTGCGCGCGTGGTGCAGACGC 997
317 nAlaIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrP 334
998 CCGCGCGGTTCGGAGTGGTCCCGGTGCATCAGCCCGATGTACCAGCTG 1047
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1048 CACAGG...CGCTCGGAGGCACCCCGCGCTCCCAACACTCGGCCACGA 1094
351 HisLysProLeuAlaGluGlyThrProArgSerAsnHisSerAlaGlnAs 367
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367 pSerAlaValGluAsnLeuLeuLeuSerLysAlaLysLeuValProS 384
1145 CGGAGCGCGAGCGCTCCCGGAGCAACAGTGCAGACTCCCGGACACC 1194
384 erGluArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThr 400
1195 GAGAGCAACACAGGAGCAGCAGCGGTCTTATCTACCTGACCAACCA 1244
401 GluSerAsnAsnGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHi 417
1245 CATGCGCCGACGCGCGCAACG...GTGCTGCTCAAGGAGGAGCAGCGG 1291
417 sIleAlaProHisAlaArgAsnGlyLeuSerLeuLysGluGluHisArg 434
1292 CCTACAGCTGCTGCGCGCGCTCCGAGAACTCGCAGAGCGCTCGCG 1341
434 latyrAspLeuLeuArgAlaAlaSerGluAsnSerGlnAspAlaLeuArg 450
1342 GTGCTCAGCAGCAGCGGAGCAGATGAAGGTGTACAAAGTCCGACACTG 1391
451 valValSerThrSerGlyGluGlnMetLysValTyrLysCysGluHisCy 467
1392 CCGGGTCTCTTCTCTGATCAGTATGTACACCATCCACATGGGCTGCC 1441
467 sArgValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysH 484
1442 ACGGCTTCGCTGATCTTTTGTAGTGAACATGTGGGCTTACACAGCCAG 1491
484 sGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGln 500
1492 GACCGGTACAGTTCGTGCTGCACATAAAGCGGAGGGGACCGCTTCCA 1541
501 AspArgTyrGluPheSerSerHisIleThrArgGlyGluHisArgPheHi 517
1542 CATGAGC 1548
517 sMetSer 519

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:AA46964
seq_documentation_block:
ID: AAR46964 standard; Protein: 537 AA.
XX
AC AAR46964;

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XX 21-OCT-1994 (first entry)
DT Peptide with Ikaros protein activity.
DE Ikaros: zinc finger; protein; immune disorder; therapy; treatment;
KW corpus striatum; regulatory gene.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 536
FT /note= "Position is encoded by a stop codon in the
FT corresponding nucleotide sequence."
XX WO9406814-A.
PN 31-MAR-1994.
PD 14-SEP-1993; 93WO-US08743.
PF 14-SEP-1992; 92US-0946233.
PR (GEHO ) GEN HOSPITAL CORP.
PA Georgopoulos K;
XX WPI: 1994-118387/14.
XX N-PSDB; AAQ44980.
DR T-cell pathway regulatory gene, Ikaros - encodes family of unique
PT zinc finger proteins, useful for treating immune system disorders
XX Claim 14; Page 44-46; 112pp: English.
XX The Ikaros gene encodes a zinc finger protein which can be used in a
CC therapeutic composition to treat animals with an immune system
CC disorder. It may also be used for assessing whether a subject is at
CC risk for an immune disorder. It is of particular use in treating a
CC disorder of the corpus striatum.
XX Sequence 537 AA;

alignment_scores:
Quality: 2480.00 Length: 487
Ratio: 5.221 Gaps: 2
Percent Similarity: 97.536 Percent Identity: 95.688

alignment_block:
US-08-711-417C-165 x AAR46964 ..

Align seg 1/1 to: AAR46964 from: 1 to: 537
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138 CTCACAGAGTACAGAGTCTGCGCCAGTAATGTTAAAGTAGAGACTCAGA 187
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67 rGlyArgArgProArg.....AlaSerAsnValLysValGluThrGlnS 82
188 GTGATGAAGAGATGGCGTGTGAAATGAATGGAAGAGAAATGCTGCC 237
|||||
82 erAspGluGluAsnGlyArgAlaCysGluMetAsnGlyGluGluCysAla 98
238 GAGATTACGAATGCTTGTATGCTCGGAGAGAGAAATGAATGCTGCCA 287
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99 GluAspLeuArgMetLeuAspAlaSerGlyGluLysMetAsnGlySerHi 115
288 CAGGACCAAGCAGCTCGGCTTTGTCGGAGTGGAGGACTTCGACTTC 337
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115 sArgAspGlnGlySerSerAlaLeuSerGlyValGlyGlyIleArgLeuP 132

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338 CTAACGGAAACTAAAGTGTGATATCTGGGATCATTTGCTATCGGCGC 387
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132 roAsnGlyLysLeuLysCysAspIleCysGlyIleIleCysIleGlyPro 148
|||||
388 AATGTGCTCATGCTCACAAGAGAACACACATGGAGAACGCCCTTCCA 437
|||||
149 AsnValLeuMetValHisLysArgSerHisThrGlyGluArgProPheG1 165
|||||
438 GTCAATCATAGTCGGGGCCCTCATTTACCCAGAGGCAACCTGCTCCGCG 487
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165 nCysAsnGlnCysGlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgH 182
|||||
488 ACATCAAGCTGCTATCCGGGAGAGCCCTTCAATGCCCACCTCTGCAAC 537
|||||
182 isIleLysLeuHisSerGlyGluLysProPheLysCysHisLeuCysAsn 198
|||||
538 TAGCGCTGCCCGGGAGGACGCCCTCACTGGCCACCTGAGGAGGCACTC 587
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199 TyrAlaCysArgArgAspAlaLeuThrGlyHisLeuArgThrHisSe 215
|||||
588 CGTTGTAAACCTCAAAATGTGGATATTGCGCGGAGCTATAAACAGC 637
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215 rValGlyLysProHisLysCysGlyTyrCysGlyArgSerTyrLysGln 232
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638 GAACGTCTTTAGAGGAACATAAAGAGCGCTGCCACAACTACTTGGAAAG 687
|||||
232 rgThrSerLeuGluGluHisLysGluArgCysHisAsnTyrLeuGluSer 248
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688 ATGGGCCCTTCGGGACACTGTACCCAGTCAATTAAGAGAACTAAAGCA 737
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249 MetGlyLeuProGlyThrLeuTyrProValIleLysGluGluThrLysH 265
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738 CAGTGAATGCGAGAAGACCTGCTCAAGATAGGATCAGAGATCTCTCG 787
|||||
265 sSerGluMetAlaGluAspLeuCysLysIleGlySerGluArgSerLeu 282
|||||
788 TGCTGGACAGACTAGCAAGTAATGTCGCCAAAGTAAAGAGCTCTATGCG 837
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282 alLeuAspArgLeuAlaSerAsnValAlaLysArgLysSerSerMetPro 298
|||||
838 CAGAAATTTCTGGGACAGAGGCTCTCCGACACGCCCTTACACAGTGC 887
|||||
299 GlnLysPheLeuGlyAspLysGlyLeuSerAspThrProTyrAspSerAl 315
|||||
888 CACGTACGAGAGAGAACGAAATGATGAAGTCCACACGTGATGGACCAAG 937
|||||
315 aThrTyrGluLysGluAsnGluMetLysSerHisValMetAspGlnA 332
|||||
938 CCATCAACAACGCCATCACTACTCGGGGGCCGAGTCCCTGCGCCCGCTG 987
|||||
332 lalleAsnAsnAlaIleAsnTyrLeuGlyAlaGluSerLeuArgProLeu 348
|||||
988 GTGACAGACGCCCGGGCGGTTCCGAGGTGGTCCGCGTCACTCAGCCGAT 1037
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349 ValGlnThrProGlyGlySerGluValValProValIleSerProMe 365
|||||
1038 GTACAGCTCCACAGCGCTCGAGGGCACCCCGCGCTCCAACCACTCGG 1087
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365 tTyGlnLeuHisArgArgSerGluGlyThrProArgSerAsnHisSerA 382
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382 lagLAspSerAlaValGluTyrLeuLeuLeuLeuSerLysAlaLysLeu 398
|||||
1138 GTCCCTCGGAGCGGAGCGGTCCTCCGAGCAACAGCTGCCAAGACTCCAC 1187
|||||
399 ValProSerGluArgGluAlaSerProSerAsnSerCysGlnAspSerTh 415
|||||
1188 GGACACCGAGACACACAGGAGGACCGGAGCGGCTTTATCTACCTGA 1237
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415 rAspThrGluSerAsnAsnGluGluGlnArgSerGlyLeuIleTyrLeu 432

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449 ArgAlaTyrAspLeuValArgAlaAlaSerGluAsnSerGlnAspAlaPh 465
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465 eArgValValSerThrSerGlyGluGlnMetLysValTyrLysCysGluH 482
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1388 ACTGCGGCTGCTCTCTGATCAGCTCATCTGACCATCATCCATGGG 1437
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482 iCysArgValLeuPheLeuAspHisValMetTyrThrIleHisMetGly 498
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1438 TGCCACGCGCTCCGTGATCCTTTTGAAGTCAACATGTGCGGTACACAG 1487
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1538 TCCACATGAGC 1548
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532 heHisMetThr 535

seq_name: /STDs1/gcsgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AA92015
seq_documentation_block:
ID AA92015 standard; Protein; 461 AA.
XX
AC AA92015;
XX
DT 09-MAY-1996 (first entry)
XX
DE Human Ikaros protein hik-1.
XX
KW Ikaros; transgene; transgenic animal; transgenic mouse; hik-1;
KW immunocompromised; immune system disorder; nervous system disorder;
KW animal model.
XX
OS Homo sapiens.
XX
PN WO9604372-A1.
XX
PD 15-FEB-1996.
XX
PF 28-JUL-1995; 95WO-US09345.
XX
PR 29-JUL-1994; 94US-0283300.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Georgopoulos K;
XX
DR WPI; 1996-129389/13.
XX
DR N-PSDB; AAT16060.
XX
PT Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
PT severely immuno-compromised and can be used as model to determine
PT effects of treatment for immune and nervous system disorders
XX
PS Disclosure; Fig 2; 102pp; English.
XX
CC An almost full-length cDNA sequence (AAT16060) codes for part
CC (AA92015) of the human Ikaros protein, a zinc finger protein that is
CC a master regulator of haematopoietic differentiation and a major
CC determinant in lymphocyte specification and development. Different
CC isoforms (see AA92014 and AA92016-19) of mouse Ikaros have also been
CC isolated. Transgenic animals, pref. mice, having a mutated Ikaros
CC transgene, esp. a mutation that alters the DNA binding domain of the

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Wed Aug 28 10:05:31 2002

CC Ikaros protein, are used as models to determine the effects of
 CC treatments for immune or nervous system disorders.

XX
 SQ Sequence 461 AA;

alignment_scores:
 Quality: 2467.00 Length: 461
 Ratio: 5.351 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-711-417c-165 x AAR92015 ..

Align seg 1/1 to: AAR92015 from: 1 to: 461

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216 AATGAATGGGAAGAAATGCGGAGGATTTACGAATGCTTGTATGCTCGG 265
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17 uMeAsnGlyGluGluCysAlaGluAspLeuA-gMetLeuAspAlaSerG 34
|||||
266 GAGAGAAATGAATGGTCCACAGGACCAAGGAGCTCGGCTTTGTCTG 315
|||||
34 LyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
|||||
316 GGAGTTGGAGCATTGCACTTCCTAACGGAAACTAAAGTGTGATATCTG 365
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51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
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366 TGGGATCATTTGTCATCGGGCCCAATGTGCTCATGTTTCACAAAGAGCC 415
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67 scGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
|||||
416 ACACCTGGAGAACGCCCTTCAGTGCATCATAGTCGGGGCTCATTCACC 465
|||||
84 IsThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
|||||
466 CAGAAAGGCAACCTCTCCCGCACATCAAGTGCATTCCGGGGAGAGCC 515
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101 GlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGluLysPr 117
|||||
516 CTTCAATGCCACCTCTGCACTAGCCTCGCGCGGAGGACGCCCTCA 565
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117 oPheLysCysHisLeuCysAsnTyAlaCysArgArgAspAlaLeuT 134
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|||||
184 alIleLysGluThrLysHisSerGluMetAlaGluAspLeuLysCys 200
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217 aLysArgLysSerSerMetProGlnLysPheLeuGlyAspLysGlyLeu 234
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866 CCGACACGCCCTACGACAGTGCACCTAGCAGAAAGGAGAACGAAATGATG 915

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301 ThrProArgSerAsnHisSerAlaGlnAspSerAlaValGluTyRLeu 317
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1116 GCTGCTCTCCAAAGCCCAAGTTGCTGCCCTCGGAGCGGAGGCGTCCC 1165
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317 uLeuLeuSerLysAlaLysLeuValProSerGluArgGluAlaSerPro 334
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434 ysAsnMetCysGlyTyRHisSerGlnAspArgTyRLeuPheSerSerHis 450
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451 IleThrArgGlyGluHisArgPheHisMetSer 461
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seq_documentation_block:
ID AAW72672 standard; Protein; 461 AA.
XX
AC AAW72672;
XX
DT 14-JAN-1999 (first entry)
XX
DE Human Ikaros.
XX
KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
KW differentiation marker; immune system; corpus striatum; AIDS;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5824770-A.

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XX

PD 20-OCT-1998.

XX

PF 05-JUN-1995; 95US-0465590.

XX

PR 02-MAY-1994; 94US-0238212.

PR

PR 14-SEP-1992; 92US-0946233.

PR

PR 14-SEP-1993; 93US-0121438.

PR

XX 05-JUN-1995; 95US-0465590.

XX

(GEHO) GEN HOSPITAL CORP.

PA

XX Georgopoulos K;

XX

PI WPI; 1998-582621/49.

DR

DR N-PSDB; AAV66969.

XX

XX Ikaros poly:peptide(s) - useful for treating disorders of immune

PT

PT system or corpus striatum

XX

PS Claim 1; Column 55-58; 111pp; English.

XX

CC The present invention describes a purified peptide having at least one
 CC of the following properties: (a) it stimulates transcription of a DNA
 CC sequence under the control of a delta A element, an NFkB element or an
 CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
 CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide
 CC consensus sequence; (c) it competitively inhibits the binding of a
 CC naturally occurring Ikaros isoform to any of a delta A element, an NFkB
 CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or
 CC (e) it inhibits protein-protein interactions of transcriptional complexes
 CC formed with naturally occurring Ikaros isoforms. The proteins, provided
 CC that they stimulate gene transcription under the control of delta A
 CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
 CC inhibit protein-protein interactions of transcriptional complexes with
 CC naturally occurring Ikaros isoforms, can be used to treat immune system
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
 CC Alzheimer's disease. The present sequence represents a specifically
 CC claimed human Ikaros protein.

XX

SQ Sequence 461 AA;

alignment_scores:

Quality: 2467.00 Length: 461
 Ratio: 5.351 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-711-417C-165 x AAW72672 ..

Align seg 1/1 to: AAW72672 from: 1 to: 461

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216 AATGAATGGGAAGATGTGCGGAGGATTTACGAATGCTTGATGCTCGG 265
 |||||

17 uMeAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
 |||||

266 GAGAGAAATGAATGGTCTCCAGGAGCAAGGAGGAGCTCGGCTTTGTGCG 315
 |||||

34 lyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
 |||||

316 GGAGTTGGAGGCAATTCAGCTTCTTACCGAAACATAAGTGTGATATCTG 365
 |||||

51 GlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAspIleCy 67
 |||||

366 TGGGATCATTTGGCATCGGGCCCAATGTGCTCATGTTTCAAAAGAAGCC 415
 |||||

67 sGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
 |||||

416 ACATGGAGAAACGGCCCTTCCAGTGAATCAGTGGCGGCGCTCATTCACC 465
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84 isThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSerPheThr 100
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134 hrGlyHisLeuArgThrHisSerValGlyLysProHisLysCysGlyTyr 150
 |||||

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716 TCATTAAAGAAACTAAGCACAGTGAATTTGGGAGAGAGCTGTGCAAG 765
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184 alIleLysGluGluThrLysHisSerGluMetAlaGluAspLeuLys 200
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766 AFAGGATCAGAGAGATCTCTCGTCTGGACAGACTAGCAAGTATGTCCG 815
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201 IleGlySerGluArgSerLeuValLeuAspArgLeuAlaSerAsnValAl 217
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816 CAAAGCTAAGAGCTCTATGCTCCTCAGAATTTCTTGGGACAAGGCCCTGT 865
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Wed Aug 28 10:05:31 2002

1266 CGTGTGCTCAAGGAGCAGCGCGCTTACGACCTGCTGCGCGCGCT 1315
 367 gValSerLeuLysGluGluHisArgAlaTyrAspLeuLeuArgAlaAs 384
 1316 CCGAAGAACTCGCAGGAGCGGCTCCGGTGGTCCAGCAGCGGGGAGCAG 1365
 384 erGluAsnSerGlnAspAlaLeuArgValValSerThrSerGlyGluGln 400
 1366 ATGAGGTGTACAGTCCGACACTCCCGGGTCTCTTCCCTGGATCAGT 1415
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 1416 CATGTACACCATCCATGGCTGGCCAGCGCTCCGTGATCCTTTTGAGT 1465
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 434 ysAsnMetCysGlyTyrHisSerGlnAspArgTyrGluPheSerHis 450
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 451 llehrArgGlyGluHisArgPheHisMetSer 461

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seq_documentation_block:

ID_AAW70964 standard; Protein; 461 AA.

AC AAW70964;

XX 11-JAN-1999 (first entry)

XX Human Ikaros isoform hlk-1.

XX Ikaros; hlk-1; transcription factor; human; lymphocyte;
 KW cell differentiation; T cell; cancer; immunodeficiency;
 KW Alzheimer's disease; therapy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH Region 64..84

FT /note= "zinc finger motif"

FT Region 92..112

FT /note= "zinc finger motif"

FT Region 120..140

FT /note= "zinc finger motif"

FT Region 148..169

FT /note= "zinc finger motif"

FT Region 406..426

FT /note= "zinc finger motif"

FT Region 434..456

FT /note= "zinc finger motif"

XX CA2194256-A.

XX 05-MAR-1998.

XX 02-JAN-1997; 97CA-2194256.

XX 05-SEP-1996; 96US-0711417.

XX (GEO) GEN HOSPITAL CORP.

XX Georgopoulos K;

XX WPI; 1998-378292/33.

XX N-PSDB; AAV42806.

XX New nucleic acid encoding Ikaros protein involved in early
 PT differentiation of lymphocytes - existing in several isoforms, and
 PT related products, used to treat e.g. immune diseases or cancer and

PT to control cell differentiation

XX Claim 7; Page 70-72; 158pp; English.

XX This is the amino acid sequence of human Ikaros protein isoform
 CC hlk-1, deduced from a cDNA clone (see AAV42806) obtained from a
 CC Jurkat T cell line cDNA library. Native Ikaros is active in the
 CC early stages of lymphocyte differentiation, binding to and
 CC activating the CD3-delta gene enhancer (see AAV42804). Proteins
 CC of the human Ikaros family (see also AAW70969 and AAW70971) are
 CC isoforms that arise from differential splicing of Ikaros gene
 CC transcripts, and contain different combinations of zinc fingers.
 CC They are expressed primarily in T cells in the adult and may play a
 CC role as a genetic switch regulating entry into the T cell lineage.
 CC The human and murine sequences (see also AAW70963 and AAW70965-68) are
 CC very similar. The invention provides Ikaros nucleic acids, vectors
 CC and host cells expressing Ikaros polypeptides. These can be used
 CC to treat T and B cell diseases (e.g. immune deficiencies caused by
 CC drugs, radiation or cancer), to control expression of heterologous
 CC genes placed under control of an Ikaros-responsive element, to
 CC treat nervous system diseases (e.g. Alzheimer's disease), and to
 CC modulate cell division, amplification or differentiation, especially
 CC in haematopoietic cells. Some Ikaros isoforms are antagonistic of
 CC others and may be used to inhibit interaction with DNA sequences.

XX Sequence 461 AA;

alignment_scores: Quality: 2454.00 Length: 461
 Ratio: 5.335 Gaps: 0
 Percent Similarity: 99.783 Percent Identity: 99.349

alignment_block:

US-08-711-417C-165 x AAW70964 ..

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 17 uMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspAlaSerG 34
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 34 lylGluLysMetAsnGlySerHisArgAspGlnGlySerSerAlaLeuSer 50
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 67 sGlyIleIleCysIleGlyProAsnValLeuMetValHisLysArgSerH 84
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 1416 CATGTACACATCCATGCGCTGCGCACGCTTCCGCTGATCTCTTTGAGT 1465
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 ID AAR92017 standard; Protein; 518 AA.
 XX AAR92017;
 AC AAR92017;
 XX 09-MAY-1996 (first entry)
 DT Murine Ikaros protein mIk-1.
 DE Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
 KW immunocomprised; immune system disorder; nervous system disorder;
 KW animal model; mIk-1.
 XX Mus musculus.

Key	Location/Qualifiers
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FT	/note= "zinc finger domain F1"
Domain	147..167
FT	/label= F2
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Domain	203..224
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Domain	460..480
FT	/label= F5
FT	/note= "zinc finger domain F5"
Domain	491..513
FT	/label= F6
FT	/note= "zinc finger domain F6"

W09604372-A1.

15-FEB-1996.

28-JUL-1995; 95WO-US09345.

29-JUL-1994; 94US-0283300.

(GEO) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1996-129389/13.

N-PSDB; T016062.

Transgenic rodent having Ikaros trans-gene (pref. mutated) - is severely immuno-compromised and can be used as model to determine effects of treatment for immune and nervous system disorders

Disclosure; Fig 4; 102pp; English.

The sequence of 57.5 kDa mouse Ikaros protein mIk-1 (AAR92017) was deduced from mouse Ikaros cDNA (AAR16062) isolated from a mature T-cell line E15 library. Ikaros protein is a master regulator of hematopoietic differentiation and a major determinant in lymphocyte differentiation. Other isoforms of Ikaros (see AAR92014, AAR92016 and AAR92018-19) arise from differential splicing of Ikaros gene transcripts. transgenic animals, esp. mice, having a mutated Ikaros transgene, esp. a mutation that alters the DNA binding domain of the Ikaros protein, are used as models to determine the effects of treatments for immune or nervous system disorders.

XX

SQ Sequence 518 AA;

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Quality: 2437.00 Length: 521
Ratio: 4.913 Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635

alignment_block:

US-08-711-417c-165 x AAR92017 ..

Align seg 1/1 to: AAR92017 from: 1 to: 518

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101 CCGAGGACCTCTCCACCACCTCGGAGGACAGCAAAAGCTCCAAGAGTGAC 150
34 roGluAspLeuSerThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGACTGCTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAA 200
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
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67 nGlyArgAlaCysGluMetAsnGlyGluGlyCysAlaGluAspLeuArg 84
251 TGCTTGATGCTCGGGAGAGAAATGAATGGCTCCACAGGGACCAAGGC 300
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
301 AGCTCGCTTTGTCGGAGTTGAGGATTCGACTTCCTTAACGGAAACT 350
101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTATATCTGTGGGATCATTTGTCATCGGGCCCAATGTGCTCATGS 400
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217 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProG 234
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seq_documentation_block:

ID AAW72674 standard; Protein; 518 AA.

XX

AC

AAW72674;

XX

DT

14-JAN-1999 (first entry)

XX

DE

Mouse Ikaros mIk-1.

XX

KW

CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia; differentiation marker; immune system; corpus striatum; AIDS; Alzheimer's disease.

XX

KW

XX

OS

Mus sp.

XX

PN

US5824770-A.

XX

PD

20-OCT-1998.

XX

XX

05-JUN-1995; 95US-0465590.

XX

PR

02-MAY-1994; 94US-0238212.

XX

PR

14-SEP-1992; 92US-0946233.

XX

PR

14-SEP-1993; 93US-0121438.

XX

PR

05-JUN-1995; 95US-0465590.

XX

XX

(GEHO) GEN HOSPITAL CORP.

XX

PI

Georgopoulos K;

XX

DR

WPI; 1998-582621/49.

XX

DR

N-PSDB; AAV66971.

XX

PT

Ikaros poly:peptide(s) - useful for treating disorders of immune system or corpus striatum

XX

PT

XX

PS

Claim 1; Column 61-66; 11pp; English.

XX

CC

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (e) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides. competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides. inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence represents a specifically claimed mouse Ikaros protein.

XX

Sequence 518 AA;

alignment_scores:

Quality: 2437.00

Length: 521

Ratio: 4.913

Gaps: 6

Percent Similarity: 95.202

Percent Identity: 89.635

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US-08-711-417C-165 x AAW72674 ..

Align seg 1/1 to: AAW72674 from: 1 to: 518

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seq_documentation_block:
ID_AAW70966 standard; Protein; 518 AA.
XX AC AAW70966;
XX DT 11-JAN-1999 (first entry)
XX DE Mouse Ikaros isoform mIk-1.
XX Ikaros; mIk-1; transcription factor; mouse; lymphocyte;
KW cell differentiation; T cell; cancer; immunodeficiency;
KW Alzheimer's disease; therapy; diagnosis.
XX OS Mus sp.
XX Key Location/Qualifiers
FH 119..139
FT Region /note= "zinc finger motif"

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147..167
/Note= "zinc finger motif"
175..195
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203..224
/Note= "zinc finger motif"
460..480
/Note= "zinc finger motif"
491..513
/Note= "zinc finger motif"

CA2194256-A.
05-MAR-1998.
02-JAN-1997; 97CA-2194256.
05-SEP-1996; 96US-0711417.
(GEHO ) GEN HOSPITAL CORP.
Georgopoulos K;
WPI; 1998-378292/33.
N-PSDB; AAV42808.

New nucleic acid encoding Ikaros protein involved in early
differentiation of lymphocytes - existing in several isoforms, and
related products, used to treat e.g. immune diseases or cancer and
to control cell differentiation

Claim 7; Page 75-77; 158pp; English.

This is the amino acid sequence of murine Ikaros protein isoform
mIk-1, deduced from a cDNA clone (see AAV42808) obtained from a
mature murine T cell line E14 library. Native Ikaros is active
in the early stages of lymphocyte differentiation, binding to and
activating the CD3-delta gene enhancer (see AAV42804). Proteins
of the murine Ikaros family (see also AAW70963 and AAW70965-68) are
isoforms that arise from differential splicing of Ikaros gene
transcripts, and contain different combinations of zinc fingers.
They are expressed primarily in T cells in the adult and may play a
role as a genetic switch regulating entry into the T cell lineage.
The murine and human sequences (see AAW70964, AAW70969 and AAW70971) are
very similar. The invention provides Ikaros nucleic acids, vectors
and host cells expressing Ikaros polypeptides. These can be used
to treat T and B cell diseases (e.g. immune deficiencies caused by
drugs, radiation or cancer), to control expression of heterologous
genes placed under control of an Ikaros-responsive element, to
treat nervous system diseases (e.g. Alzheimer's disease) and to
modulate cell division, amplification or differentiation, especially
in haematopoietic cells. Some Ikaros isoforms are antagonistic of
CC others and may be used to inhibit interaction with DNA sequences.
XX Sequence 518 AA;
SQ

alignment_scores:
Quality: 2437.00 Length: 521
Ratio: 4.913 Gaps: 6
Percent Similarity: 95.202 Percent Identity: 89.635

alignment_block:
US-08-711-417C-165 x AAW70966 ..
Align seg 1/1 to: AAW70966 from: 1 to: 518
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|||||
1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGlu 17
|||||
51 CCCCCCTGTAAAGCGATACTCCAGATGAGGCGGATGAGCCCATGCCATCC 100
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17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CGAGGACCTTCCACCACTCGGGAGGACAGCAAAAGCTCAAGAGTGAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 AGAGTCGTGGCCAGTAAAGTTAAAGTAGAGACTCAGAGTGAAGAGAA 200
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51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
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201 TGGCGCTGCCTGTGAATGAATGGGAAGAATGTGCGAGGATTACGAA 250
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67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgm 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 TGCTTGATGCTCGGGAGAGAAATGAATGCTCCACAGGGACCAAGGC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 AGCTCGGCTTTCTCGGGAGTTGGAGGCATTGCACTTCCCTAACGGAAACT 350
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101 SerSerAlaLeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
401 TTCACAAAGAGGACCACTGGAGAACGGCCCTTCCAGTCAATCAGTGC 450
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134 aHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150
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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
751 GAAGACTGTGCAAGTAGATCAGACAGAGATCTCTGCTGTCGACAGACT 800
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266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283
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300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 315
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315 alleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 332
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1051 AGG...CGTCCGAGGAGCCCGCGCTCCAACTCCGCGCCAGGACAG 1097
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349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 364
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365 .AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerg 381
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381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
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1198 AGCAACACAGGAGGACGCGCGCTGCTATCTACCTGACCAACACCAT 1247
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398 SerAsnAlaGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIl 414
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431 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
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448 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 464
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1395 GGTGCTCTTCTGATCAGCTCATGTACACATCCACATG.....G 1435
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464 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 481
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1436 GCTCCGACGCTTCCGTGATCCCTTTTTCAGTGCACATGTGGGTACAC 1485
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481 lyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 497
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seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT: AAR46965
seq_documentation_block:
ID AAR46965 standard; Protein; 568 AA.
XX
AC AAR46965;
XX
XX 21-OCT-1994 (first entry)
XX
DE Ikaros zinc finger protein isoform IK-1.
XX
XX Ikaros; zinc finger; protein; immune disorder; therapy; treatment;
KW korpus striatum; regulatory gene.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1..53
FT Exon 1/2.
FT Region 54..141
FT Exon 3.
FT Region 142..247
FT Exon 4.
FT Region 248..288
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FT /label= Exon 5.
 FT 289..333
 FT /label= Exon 6.
 FT 334..568
 FT /label= Exon 7.
 XX
 PN W09406814-A.
 XX
 XX 31-MAR-1994.
 PD
 XX 14-SEP-1993; 93WO-US08743.
 PF
 XX 14-SEP-1992; 92US-0946233.
 PR
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 XX Georgopoulos K;
 PI
 XX WPI; 1994-118387/14.
 DX
 XX

XX T-cell pathway regulatory gene, Ikaros - encodes family of unique
 PT zinc finger proteins, useful for treating immune system disorders
 PT
 PS Claim 14; Figure 4; 112pp; English.
 XX

CC The Ikaros gene encodes a zinc finger protein which can be used in a
 CC therapeutic composition to treat animals with an immune system
 CC disorder. It may also be used for assessing whether a subject is at
 CC risk for an immune disorder. It is of particular use in treating a
 CC disorder of the corpus striatum.
 XX

SQ Sequence 568 AA;

alignment_scores:
 Quality: 2422.00 Length: 571
 Ratio: 4.863 Gaps: 7
 Percent Similarity: 87.215 Percent Identity: 82.137

alignment_block:

US-08-711-417C-165 x AAR46965 ..

Align seg 1/1 to: AAR46965 from: 1 to: 568

1 ATGATGCTGACGAGGTCAAGACATGCTCTTCATCAGGGAGGAAAG 50
 1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
 51 CCCCCCTGTAAGCGATACCTCCACACCTCGGAGGACAGCAAAAGCTCCAGAGTGAC 100
 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
 101 CCGAGGACCTCTCCACACCTCGGAGGACAGCAAAAGCTCCAGAGTGAC 150
 34 roGluAspLeuSerThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
 151 AGAGTCGTGCCAGTATGTTAAAGTAGACACTCAGAGTCAGTGAAGAGAA 200
 51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
 201 TGGGCGTGCCTGTGAATGAATGGGGAAGAATGTGCGGAGGATTTACGAA 250
 67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
 251 TGCTTGATGCTCGGAGAGAAATGAATGGTCTCCACAGGAGCAAGGC 300
 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgaspGlnGly 100
 300 300
 101 SerSerAlaLeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLe 117
 300 300

117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
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 134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnCys 150
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 151 SerSerAlaLeuSerGlyValGlyIleArgLeuProAsnGlyLysLe 167
 351 AAAGTGTGATATCTGTGGATCATTTGTCATCGGCCCAATGTGCTCATGS 400
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 701 GCACACTGTACCCAGTCATTAAAGAGAACTAAGCAGACAGTGAATGCA 750
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 300 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 316
 801 AGCAAGTAAATGTGCGCAACCGTAGAGCTCTATGCTCAGAAATTTCTTG 850
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 1147 1147

415 AlaValAspAsnLeuLeuLeuLeuSerLysAlaLysSerValSerSerG 431
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 1248 CGCCGAGCGCGCAACGC...GTGTGCTCAAGGAGGAGCGCGCCT 1294
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 1436 GCTGCCAGCGTCCGTCATCTTTTTCAGTGCACATGTCGGGTACAC 1485
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seq_documentation_block:

ID AAR92021 standard; Protein; 470 AA.

AC AAR92021;

DT 09-MAY-1996 (first entry)

XX Ikaros protein.

XX Ikaros; transgene; transgenic animal; transgenic mouse; lymphocyte;
 KW immunocomprised; immune system disorder; nervous system disorder;
 KW animal model.

XX Not specified.

XX Key Location/Qualifiers

FH Misc-difference 1..2 /note= "unidentified amino acids"
 FT Misc-difference 74 /note= "unidentified amino acid"
 FT Misc-difference 163 /note= "unidentified amino acid"
 FT Misc-difference 184..186 /note= "unidentified amino acids"
 FT Misc-difference 194 /note= "unidentified amino acid"
 FT Misc-difference 196 /note= "unidentified amino acid"
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 FT Misc-difference 236 /note= "unidentified amino acid"
 FT Misc-difference 240

FT Misc-difference 246 /note= "unidentified amino acid"
 FT Misc-difference 251..252 /note= "unidentified amino acids"
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 FT Misc-difference 407 /note= "unidentified amino acid"
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 FT Misc-difference 467 /note= "unidentified amino acid"
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 FT WO9604372-A1.
 XX 15-FEB-1996.
 XX 28-JUL-1995; 95WO-US09345.
 XX 29-JUL-1994; 94US-0283300.
 XX (GEHO) GEN HOSPITAL CORP.
 XX Georgopoulos K;
 XX WPI; 1996-129389/13.
 XX Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
 PT severely immuno-compromised and can be used as model to determine
 PT effects of treatment for immune and nervous system disorders
 XX Disclosure; Page 75-76; 102pp; English.
 XX The sequence of an Ikaros protein (AAR92021) is provided in the
 CC specification. Ikaros protein is a major regulator of
 CC hematopoietic differentiation and a major determinant in lymphocyte
 CC differentiation. Isoforms of Ikaros (see AAR92014-19) arise from
 CC differential splicing of Ikaros gene transcripts. Transgenic animals,
 CC pref. mice, having a mutated Ikaros transgene, esp. a mutation that
 CC alters the DNA binding domain of the Ikaros protein, are used as

CC models to determine the effects of treatments for immune or nervous
 CC system disorders.

SQ Sequence 470 AA;

alignment_scores:

Quality: 2207.50 Length: 468
 Ratio: 5.098 Gaps: 3
 Percent Similarity: 92.521 Percent Identity: 90.385

alignment_block:

US-08-711-417c-165 x AAR92021

Align seg 1/1 to: AAR92021 from: 1 to: 470

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260 CCTCGGAGAGAAATGAATGGCTCCACAGGGACCAAGGAGCTCGGT 309
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36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
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53 LeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCATTCGGGCCCAATGTGCTCATGTTTCAAAA 409
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69 pileCysGlyLeu***CysIleGlyProAsnValLeuMetValHisLysA 86
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86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
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510 GAAGCCCTCAATGCACTGCACTGCACTGCACTGCACTGCACTGCACT 559
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660 AGAGCGCTGCCAACACTACTTGAAGAGCATGGCCCTTCGGGGCAGACTGT 709
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169 sGluArgCysHisAsnTyrLeuGlnSerMetGlyLeuProGly***** 186
710 ACCAGCTCATTAAGAGAACTAAGACAGTGAATGGCAGAAGACCTG 759
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203 CysLysIleGly**GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTGCGCAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGGACAGG 859
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860 GCCTGTCCGACACGCCCTACGACAGTGCACGTACGAGAAGGAGAAGCAA 909

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253 MetMet***SerHisValMetAsp***AlaIleAsnAsnAlaIleAsnTy 269
960 CTTGGGGGGCGAGTCCCTGCGGCCGCTGTGTGTGTGTGTGTGTGTGTGT 1009
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269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProProGly***S 286
1010 CCGAGGTGTCTCCCGGTCTATCAGCCGATGTACCAGCTGCAC...AGGCGC 1056
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286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGGAGGACACCCCGGCTCCAAACACTCGGCCAGGACAGCGCGGTGGA 1106
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303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGCTGCTCTCCCAAGGCCAAGTTGGTGCCTCGGAGCGCGAGG 1156
|||||
319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
1157 CTTCCCGGAGCAACAGCTGCCAAGACTCCACGAGCACGAGAGCAACAAC 1206
|||||
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
1207 GAGGAGCAGCGAGCGGTCTTATCTACCTGACCAACACATCGCCCGCAG 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CCGC...CAACGCGTGTGCTCAAGGAGGACGCGCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaLys*****L 386
1304 TCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCCGCGTGTGTGTGTGT 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
1354 AGCGGGGAGCAGATGAAGTGTACAAAGTGCAGAACACTGCGCGGTCTCTT 1403
|||||
403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
1404 CTTGATCAGCTCATGTACACCATCCACATG.....GGCTGCCACG 1444
|||||
419 eleuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCCGTGATCCTTTTGAGTGCACATGTGCGGTACCCAGCCAGGAC 1494
|||||
436 lypHeArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCTCTGTCGCACATACGCGAGGAGGAGCAGCGCTTCCACAT 1544
|||||
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
|||||
469 *Ser 470

```

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW72678

seq_documentation_block:

ID AAW72678 standard; Protein; 470 AA.

XX

XX AAW72678;

XX

DT 14-JAN-1999 (first entry)

XX

DE Ikaros protein general formula.

XX

XX CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;

KW differentiation marker; immune system; corpus striatum; AIDS;

KW Alzheimer's disease.

FT			/note=	"any amino acid"
FT	Misc-difference	374	/note=	"any amino acid"
FT	Misc-difference	375	/note=	"any amino acid"
FT	Misc-difference	380	/note=	"any amino acid"
FT	Misc-difference	384	/note=	"any amino acid"
FT	Misc-difference	385	/note=	"any amino acid"
FT	Misc-difference	397	/note=	"any amino acid"
FT	Misc-difference	407	/note=	"any amino acid"
FT	Misc-difference	430	/note=	"any amino acid"
FT	Misc-difference	431	/note=	"any amino acid"
FT	Misc-difference	432	/note=	"any amino acid"
FT	Misc-difference	467	/note=	"any amino acid"
FT	Misc-difference	469	/note=	"any amino acid"
FT			/note=	"any amino acid"
PN	US5824770-A.			
XX	20-OCT-1998.			
XX	05-JUN-1995;	95US-0465590.		
XX	02-MAY-1994;	94US-0239212.		
PR	14-SEP-1992;	92US-0946233.		
PR	14-SEP-1993;	93US-0121438.		
PR	05-JUN-1995;	95US-0465590.		
XX				
XX	(GEOH) GEN HOSPITAL CORP.			
XX	Georgopoulos K;			
XX	WPI; 1998-582621/49.			
XX	Ikaros poly:peptide(s) - useful for tre			
PT	system or corpus striatum			
XX	Claim 1; Column 127-130; 111pp; English			
PS				
XX	The present invention describes a purifi			
CC	of the following properties: (a) it st			
CC	sequence under the control of a delta			
CC	Ikaros binding oligonucleotide consensu			
CC	a delta A element, an NFkB element or a			
CC	consensus sequence; (c) it competitivel			
CC	naturally occurring Ikaros isoform to a			
CC	element or an Ikaros binding oligonucle			
CC	competitively inhibits Ikaros binding t			
CC	(e) it inhibits protein-protein interact			
CC	formed with naturally occurring Ikaros			
CC	that they stimulate gene transcription			
CC	elements, NFkB elements and/or Ikaros-b			
CC	delta A elements, NFkB elements and/or			
CC	competitively inhibit binding of natura			
CC	delta A elements, NFkB elements and/or			
CC	competitively inhibit Ikaros binding to			
CC	inhibit protein-protein interactions of			
CC	naturally occurring Ikaros isoforms, c			
CC	disorders, e.g. leukaemia or AIDS, or			
CC	Alzheimer's disease. The present sequen			
CC	general formula from the present inven			
XX	Sequence	470 AA;		
SQ				

alignment_scores:

Quality: 2207.50 Length: 468
 Ratio: 5.098 Gaps: 3
 Percent Similarity: 92.521 Percent Identity: 90.385

alignment_block:

US-08-711-417C-165 x AAW72678 ..

Align seg 1/1 to: AAW72678 from: 1 to: 470

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|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
210 CTGTGAAATGAATGGGGAAGATGTCGCGAGGATTTACGAATGCTTGATG 259
|||||
19 acysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
260 CCTCGGAGAGAAATGAATGGTCCACAGGACCAAGGACGAGCTCGGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTCTGGGATCATTTGCATFCGGGCCCAATGTGCTCATGTTTACAAAA 409
|||||
69 pillecysglytile***cystileGlyProAsnValLeuMetValHisLysA 86
410 GAAGCCACACTGGAGAGAGCCCTTCCAGTGCATCAATCAGTCGGGGCTCA 459
|||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCCAGAGGCAACCTGCTCCGCGACATCAAGCTGCATTCCTCCGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
510 GAAGCCCTTCAATGCACTCTGCAACTACGGCTGCGCGCGAGGAGCG 559
|||||
119 ulysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136
560 CCTCTACTGCGCCACTCAGGACGACCTCCGCTGTGTAACCTCAAAATGT 609
|||||
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGCGCGAAGCTATAACAGCGCAACGCTCTTTAGAGGAACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg***SerLeuGluGluHisLy 169
|||||
660 AGAGCGCTGCCACACTACTTGGAAAGCATGGCCCTTCGGGGCACACTGT 709
|||||
169 sGluArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGCTATTAAAGAAAGAACTTAAGCAGTGAATGGCAGAGACCTG 759
|||||
186 **ProValIleLysGluGluThr***His***GluMetAlaGluAspLeu 202
760 TGCAGATAGGATCAGAGAGATCTCTGCTGCTGGAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly***GluArgSerLeuValLeuAspArgLeuAlaSerAs 219
810 TGTGCGCAACGTAAGAGCTCTATGCCTCAGAAATTTCTTGGGGACAAGG 859
|||||
219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCTGTCCGACACGCGCTACGACAGTGCACGCTACGAGAGGAAACGAA 909
|||||
236 **LeuSerAsp***ProTyrAspSerAla***TyrGluLysGlu***** 252
910 ATGATGAAGTCCCGATGATGACCAAGCCATCAACACGCGCATCACTA 959
|||||

```

```

253 MetMet***SerHisValMetAsp***AlaIleAsnAsnAlaIleAsnTy 269
960 CTGGGGGCGAGTCCCTCGCCCGCTGTGTGCAGACCCCGCGGGGT 1009
|||||
269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProGly***S 286
1010 CCGAGGTGTCCCGGTATCATCAGCCCGATGTACCAGCTGCAC...AGCGC 1056
|||||
286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGAGGCGCACCCCGCGCTCCCAACCACTCGGCCAGGACAGCGCGTGA 1106
|||||
303 Ser***Gly***ProArgSerAsnHisSerAlaGlnAsp***AlaVal** 319
1107 GTACCTGTCTGCTCTCTCCAAAGCCAAAGTTGTGCTCGGAGCGGAGG 1156
|||||
319 ***LeuLeuLeuLeuSerLysAlaLys***Val***SerGluArgGluA 336
1157 CGTCCCGGAGCAACAGCTGCCAAGACTCCACGACGACGAGAGCAACAC 1206
|||||
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn*** 352
1207 GAGGAGCAGCGCGGTCTTATCTACCTGACCAACACCATCGCCCGAGC 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CCGG...CAACGCGTGTGCTCAAGGAGGAGCAGCGCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
1304 TCGCGCGCGCTCCGAGAACTCGCAGGACGCGCTCCGCGTGTGTACAGC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla***ArgValValSerThr 402
1354 AGCGGGGAGCAGATGAAGTGTACAAAGTGCAGAACTCCCGGGTGTCTTT 1403
|||||
403 SerGlyGluGln***LysValTyrLysCysGluHisCysArgValLeuPh 419
1404 CTGTGATCAGCTCATGTATACACCATCCACATG.....GGCTGCCACG 1444
|||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCCGTGATCCTTTTGTGTCACATGTGCGGTACCAACAGCCAGGAC 1494
|||||
436 lypheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCTGTCGCACATACCGGAGGAGGAGCAGCGCTTCCACAT 1544
|||||
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
|||||
469 *Ser 470

```

seq_name: /STDs1/gcdata/hold-geneseq/geneseq-emb1/AA1998.DAT.AAW70970

seq_documentation_block:

ID AAW70970 standard; Protein; 470 AA.

XX AC AAW70970;

XX DT 11-JAN-1999 (first entry)

XX DE Ikaros isoform 1 consensus.

XX KW Ikaros; mik-1; htk-1; transcription factor; mouse; human;
 KW lymphocyte; cell differentiation; T cell; cancer;
 KW immunodeficiency; Alzheimer's disease; therapy; diagnosis.

XX OS Mus sp.

XX FT

XX Key Location/Qualifiers
 FT Misc-difference 1

FT FT /note= "variable"
FT Misc-difference 2 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 74 /label= Gly, Ala, Val, Ile, Leu, Ser, Thr
FT FT /note= "the codon for Thr-89 may be made
FT FT degenerate to provide a stop codon in
FT FT recombinant genes of a degenerate library"
FT Misc-difference 145 /note= "the codon for Ser-145 may be made
FT FT degenerate to provide a stop codon in
FT FT recombinant genes of a degenerate library"
FT Misc-difference 163 /note= "variable"
FT FT /label= Gly, Ala, Val, Ile, Leu, Ser, Thr
FT FT /note= "residue 184 may also not be present"
FT Misc-difference 185 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 187 /note= "the codon for Pro-187 may be made
FT FT degenerate to provide a stop codon in
FT FT recombinant genes of a degenerate library"
FT Misc-difference 194 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 196 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 207 /note= "variable"
FT FT /note= "the codon for Gly-232 may be made
FT FT degenerate to provide a stop codon in
FT FT recombinant genes of a degenerate library"
FT Misc-difference 236 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 240 /note= "variable"
FT FT /note= "variable"
FT Misc-difference 246 /note= "variable"
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FT Misc-difference 285 /note= "variable"
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FT Misc-difference 300 /note= "variable"
FT FT /note= "variable"
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FT Misc-difference 352

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FT Misc-difference 368 /note= "variable"
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FT XX
FT XX CA2194256-A.
FT PN
FT XX
FT PD 05-MAR-1998.
FT XX
FT PF 02-JAN-1997; 97CA-2194256.
FT XX
FT PR 05-SEP-1996; 96US-0711417.
FT XX
FT PA (GEO) GEN HOSPITAL CORP.
FT XX
FT PI Georgopoulos K;
FT XX
FT DR WPI; 1998-378292/33.
FT XX
FT PT New nucleic acid encoding Ikaros protein involved in early
FT PT differentiation of lymphocytes - existing in several isoforms, and
FT PT related products, used to treat e.g. immune diseases or cancer and
FT PT to control cell differentiation
FT XX
FT PS Disclosure; Page 59-60; 158pp; English.
FT XX
FT CC This is an example of a potential Ikaros sequence derived from a
FT CC degenerate library of polypeptides based on the amino acid
FT CC sequences of human and murine Ikaros isoform 1 proteins hik-1 (see
FT CC AAW70964) and mtk-1 (see AAW70966). A combinatorial library is
FT CC produced using a degenerate library of genes which each include
FT CC at least a portion of potential Ikaros sequences. It can be
FT CC generated by combinatorial mutagenesis at the nucleic acid level.
FT CC Native Ikaros is active in the early stages of lymphocyte
FT CC differentiation. Different isoforms arise from differential
FT CC splicing of Ikaros gene transcripts. They are expressed primarily
FT CC in T cells in the adult and may play a role as a genetic switch
FT CC regulating entry into the T cell lineage. The invention provides
FT CC Ikaros nucleic acids (see AAW42805-11 and AAW42840), polypeptides (see
FT CC AAW70963-71), vectors and host cells. These can be used to treat T

CC and B cell diseases (e.g. immune deficiencies caused by drugs,
 CC radiation or cancer), to control expression of heterologous genes
 CC placed under control of an Ikaros-responsive element, to treat
 CC nervous system diseases (e.g. Alzheimer's disease), and to modulate
 CC cell division, amplification or differentiation, especially
 CC in haematopoietic cells. Some Ikaros isoforms are antagonistic of
 CC others and may be used to inhibit interaction with DNA sequences.
 XX

SQ Sequence 470 AA;

alignment_scores:
 Quality: 2204.50 Length: 468
 Ratio: 5.091 Gaps: 3
 Percent Similarity: 92.521 Percent Identity: 90.171

alignment_block:

US-08-711-417c-165 x AAW70970 ..

Align seg 1/1 to: AAW70970 from: 1 to: 470

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|||||
3 AlaSerAsnValLysValGluThrGlnSerAspGluGluAsnGlyArgAl 19
210 CTGTCAATGATGGGGAAGAAATGTGGGAGGATTACGAATGTTGATG 259
|||||
19 aCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgMetLeuAspA 36
260 CCTCGGGAGAGAAATGAATGGCTCCACAGGGACCAAGCAGCTCGCT 309
|||||
36 laSerGlyGluLysMetAsnGlySerHisArgAspGlnGlySerSerAla 52
310 TTGTGGGAGTTGGAGCATTCGATTCCTAACGGAAACTAAAGTGTGA 359
|||||
53 LeuSerGlyValGlyGlyIleArgLeuProAsnGlyLysLeuLysCysAs 69
360 TATCTGTGGGATCATTTGCATCGGGCCCAATGCTCATGTTTCACAAA 409
|||||
69 pIleCysGlyIle**CysIleGlyProAsnValLeuMetValHisLysA 86
410 GAAGCCACTTGGAGAACGGCCCTTCCAGTGCATCATAGTCGGGGCTCA 459
|||||
86 rgSerHisThrGlyGluArgProPheGlnCysAsnGlnCysGlyAlaSer 102
460 TTCACCCAGAAAGGCAACCTGCTCCGGCACATCAAGCTGATTCGGGGA 509
|||||
103 PheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHisSerGlyGI 119
510 GAAGCCCTTCAATGCCACCTTGCACACTACGCTCGCCCGCGAGGACG 559
|||||
119 uLysProPheLysCysHisLeuCysAsnTyrAlaCysArgArgAspA 136
560 CCTCTACTGGCCACTGAGGACCACTTCCGTTGGTAAACCTCAACATGT 609
|||||
136 laLeuThrGlyHisLeuArgThrHisSerValGlyLysProHisLysCys 152
610 GGATATTGTGGCGAGCTATAACAGCGAACGCTCTTACAGGAACATAA 659
|||||
153 GlyTyrCysGlyArgSerTyrLysGlnArg**SerLeuGluGluHisLy 169
660 AGAGCGCTGCCACAACCTACTTGAAGAGCATGGCCCTTCGGGGCACACTGT 709
|||||
169 sGlnArgCysHisAsnTyrLeuGluSerMetGlyLeuProGly***** 186
710 ACCAGCTCATTAAGAAGAACTTAACACAGTGAATGGCAGAAGACCTG 759
|||||
186 **ProValIleLysGluGluThr**His**GluMetAlaGluAspLeu 202
760 TGCAAGATAGGATACAGAGACTCTCGTGTGGAGACTAGCAAGTAA 809
|||||
203 CysLysIleGly**GluArgSerLeuValLeuAspArgLeuAlaSerAs 219

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810 TGTGCGCAAAACGTAAGAGCTCTATGCTCAGAAATTTCTTGGGACAAGG 859
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219 nValAlaLysArgLysSerSerMetProGlnLysPheLeuGlyAspLys* 236
860 GCCTGTCCGACAGCCCTACGACAGTCCACGACGTACGAGAGAGAGAA 909
|||||
236 **LeuSerAsp**ProTyrAspSerAla**TyrGluLysGlu***** 252
910 ATGATGAAGTCCACAGTGTAGTGGACCAAGCCATCAACAAGCCATCACTA 959
|||||
253 MetMet**SerHisValMetAsp**AlaIleAsnAlaIleAsnTy 269
960 CTTGGGGGCGAGTCCCTGCGCCGCTGTGTGCAGACGCCCGGGCGGTT 1009
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269 rLeuGlyAlaGluSerLeuArgProLeuValGlnThrProGly***S 286
1010 CCGAGTGTGTCGGTCTATCAGCCCGATGTACCAGCTGCAC...AGGC 1056
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286 erGluValValProValIleSerProMetTyrGlnLeuHis***** 302
1057 TCGGAGGGCACCCCGCTCCACCACTCGGCCAGGACAGCGCGTGA 1106
|||||
303 Ser**Gly**ProArgSerAsnHisSerAlaGlnAsp**AlaVal** 319
1107 GTACCTGCTGCTCTCCCAAGCCCAAGTTGTCCTCGGAGCGCGAGG 1156
|||||
319 ***LeuLeuLeuSerLysAlaLys**Val**SerGluArgGluA 336
1157 CGTCCCGGACAGCTCCAGACTCCACGAGTCCACGACACCGAGAGCAAC 1206
|||||
336 laSerProSerAsnSerCysGlnAspSerThrAspThrGluSerAsn** 352
1207 GAGGACGCGCGGCTCTTATCTACCTGACCAACACCATCGCCCGCAG 1256
|||||
353 GluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisIle***** 369
1257 CCGC...CAACGCGTGTGCTCAGGAGGAGCAGCCGCTACGACCTGC 1303
|||||
369 *Ala*****LeuLysGluGlu***ArgAlaTyr*****L 386
1304 TCGCGCGCCCTCCGAGAACTCGGAGGAGCGCTCCGCGTGTGTCAGACC 1353
|||||
386 euArgAlaAlaSerGluAsnSerGlnAspAla**ArgValValSerThr 402
1354 ACGGGGGAGCAGATGAAGTGTACAAAGTGCAGAACACTCGCGGTGCTCT 1403
|||||
403 SerGlyGluGln**LysValTyrLysCysGluHisCysArgValLeuPh 419
1404 COTGATCAGCTCATGTACACCATCCACATG.....GGCTGCCACG 1444
|||||
419 eLeuAspHisValMetTyrThrIleHisMet*****GlyCysHisG 436
1445 GCTTCCGTGATCTTTTCAGTGCACATGTGCGGTACCAAGCCAGGAC 1494
|||||
436 lPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 452
1495 CGGTACGAGTTCCTGCTCGCACAATAACGGGAGGAGCAGCCGCTTCCACAT 1544
|||||
453 ArgTyrGluPheSerSerHisIleThrArgGlyGluHisArg***His** 469
1545 GAGC 1548
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469 *Ser 470

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT: AAR92016

seq_documentation_block:

ID AAR92016 standard; Protein; 432 AA.

XX
 AC
 XX
 DT 08-MAY-1996 (first entry)
 XX


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312 SerAsnAlaGluGlnArgSerGlyLeuIleTyrLeuThrAsnHis1 328
1248 CGCCGACGCGCCCAACGC...GTGTCGCTCAAGGAGGACCGCGCT 1294
|||||
328 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlaT 345
1295 AGACCTGTGCGCGCGCTCGAGAACTCGAGGACGCGCTCCGCGTG 1344
|||||
345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361
1345 GTACGACGACGCGGAGCAGATGAGGTGTACAGTGCAGACACTGCCG 1394
|||||
362 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysar 378
1395 GTGCTCTTCTCGATCAGCTATGTACACCATCCACATG.....G 1435
|||||
378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395
1436 GTGCGCACGCGCTTCCGTGATCCCTTTTGTAGTGCAACATGTGCGCTACCCAC 1485
|||||
395 lYcysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 411
1486 AGCAGGACGCGGTACGAGTCTCGTCGCACATAACGCGGAGGACCG 1535
|||||
412 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisar 428
1536 CTCCACATGAGC 1548
|||||
428 gTyrHisLeuSer 432

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW72673

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seq_documentation_block:
ID AAW72673 standard; Protein; 432 AA.
XX AC AAW72673;
XX DT 14-JAN-1999 (first entry)
XX DE Mouse Ikaros mIk-3.
XX KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
XX KW differentiation marker; immune system; corpus striatum; AIDS;
XX OS Alzheimer's disease.
XX PN Mus sp.
XX PD US5824770-A.
XX PF 20-OCT-1998.
XX PR 05-JUN-1995; 95US-0465590.
XX PR 02-MAY-1994; 94US-0238212.
XX PR 14-SEP-1992; 92US-0946233.
XX PR 14-SEP-1993; 93US-0121436.
XX PR 05-JUN-1995; 95US-0465590.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Georgopoulos K;
XX DR WPI; 1998-582621/49.
XX DR N-PSDB; AAW66970.
XX PT Ikaros poly:peptide(s) - useful for treating disorders of immune
XX PT system or corpus striatum

```

Claim 1; Column 57-62; 111pp; English.

PS The present invention describes a purified peptide having at least one
XX of the following properties: (a) it stimulates transcription of a DNA
CC sequence under the control of a delta A element, an NFkB element or an
CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide
CC consensus sequence; (c) it competitively inhibits the binding of a
CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it
CC competitively inhibits Ikaros binding to Ikaros responsive elements; or
CC (e) it inhibits protein-protein interactions of transcriptional complexes
CC formed with naturally occurring Ikaros isoforms. The proteins, provided
CC that they stimulate gene transcription under the control of delta A
CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
CC competitively inhibit Ikaros binding to Ikaros-binding oligonucleotides,
CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
CC inhibit protein-protein interactions of transcriptional complexes with
CC naturally occurring Ikaros isoforms, can be used to treat immune system
CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
CC Alzheimer's disease. The present sequence represents a specifically
XX claimed mouse Ikaros protein.

SQ Sequence 432 AA;

alignment_scores:
Quality: 1963.00 Length: 521
Ratio: 4.776 Gaps: 6
Percent Similarity: 78.887 Percent Identity: 74.280

alignment_block:

US-08-711-417C-165 x AAW72673

Align seg 1/1 to: AAW72673 from: 1 to: 432

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1 ATGGATGCTGACGAGGTCACAGCATGTCTTCTCATCAGGAGGAAG 50
|||||
1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
51 CCCCCCTGTAAAGCATCTCCAGATGAGGGGATGAGCCCATGCCGATCC 100
|||||
17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
101 CCGAGGACCTCTCCACACCTCGGGAGGACAGCAAGCTCCAAGAGTGC 150
|||||
34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151 AGAGTCGTGGCCAGTAAATGTTAAAGTAGAGACTCAGAGTGATGAAGAA 200
|||||
51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
201 TGGCGGTGCTGTCGAATGATGGGGAAGATGTGCGGAGGATTTACGAA 250
|||||
67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgM 84
251 TGCTTTGATGCTCGGGAGAGAAAATGAATGGCTCCACAGGAGCAAGGC 300
|||||
84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgaspGlnGly 100
301 AGCTCGGCTTTGTCGGGAGTTGGAGGATTCGACTTCCTAACGGAAACT 350
|||||
101 SerSerAlaLeuSerGlyValGlyIleArgLeuProAsnGlyLysLe 117
351 AAAGTGTGATATCTGTGGATCATTTTCATCGGGGCCCAATGTCGTCATG 400
|||||
117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
401 TTCACAAAGAGCAGACTGGAGAACGGCCCTTCCAGTGCATCAATCAGTC 450
|||||
134 alHisLysArgSerHisThrGlyGluArgProPheGlnCysAsnGlnSer 150

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451 GGGGCTCATTACCCAGAGAGGCAACCTGCTCCGGCACATCAAGCTGCA 500
|||||
151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCCGGGAGAGCCCTTCAATGCCACTCTGCAACTACGCTGCCGCC 550
|||||
167 sSerGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 184
551 GGAGGAGCCCTCACTGCGCACCTGAGGAGCAGCACTCGTTGGTAAACCT 600
|||||
184 rArgAspAlaLeuThrGlyHisLeuArgThrHisSer..... 196
601 CACAAATGTGGATATTGTGGCGGAAGCTATAAACACGCAACGCTCTTTAGA 650
196 ..... 196
651 GGAACATAAAGAGCGCTGCCACAACACTTGTGAAAGCATGGCCCTTCGGG 700
196 ..... 196
701 GCACACTGTACCCAGTCATTAAAGAAGAAACTAAGCAGAGTGAATGGCA 750
196 ..... 196
751 GAAGACCTGTGCAAGATAGGATCAGAGAGATCTCTGCTGGACAGACT 800
196 ..... 196
801 AGCAAGTATGTGCCCAACGTAAGAGCTCTATGCTCAGAAATTTCTTG 850
197 .....G 197
851 GGGACAGGCGCTGTCCGACAGCCCTACGACAGTCCACGTCACGAGAAG 900
|||||
197 LysPheLysLeuSerLeuMetProTyrAspSerAlaAsnTyrGluLys 213
901 GAGAAGCAATATGATGAAGTCCACGCTGATGGACCAAGCCATCAACAACGC 950
||| :|||
214 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 229
951 CATCAACTACCTGGGGCGGAGTCCCTGCGCCGCTGGTGGCAGACGCC 1000
|||||
229 aIleAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProP 246
1001 CGGGCGGTTCCGAGGTGGTCCCGGTCATCAGCCGATGTACCAGCTGCAC 1050
|||||
246 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 262
1051 AGG...CGTTCGAGGAGCCCGCGCTCCACCAAGTGGTGGCCCTCGG 1097
::: |||
263 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 278
1098 CGCGGTGGAGTACTGCTGCTCTCCAGGCCAAGTGGTGGCCCTCGG 1147
|||||
279 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 295
1148 AGCGCAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGACACCGAG 1197
|||||
295 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 311
1198 AGCAACACGAGGAGCAGCGCGCTTCTTATCTACTGACCAACACAT 1247
|||||
312 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 328
1248 CGCCCGAGCGCGCAACGC...GTGCTGCTCAGGAGGAGCAGCGCCCT 1294
| :|||
328 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlar 345
1295 ACGACCTGCTGCGCGCGCTCCGAGAATCTCGCAGGAGCAGCGCTCCGCGTG 1344
|||||
345 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 361

```

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1345 GTCAGCACCGCGGGGAGCAGATGAAGTGTACAAGTCCGAACACTGCCG 1394
|||||
362 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 378
1395 GGTGCTCTTCTCGATCCACGTCATGTACACCATCCACATG.....G 1435
|||||
378 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 395
1436 GCTGCCACGCGTCCCGTGTATCTTTTGAAGTCAACATGTCCGGCTACCCAC 1485
|||||
395 LysCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrHis 411
1486 AGCAGACCGGTCAGAGTTCTGTCGCACATACCGGAGGAGGACCG 1535
|||||
412 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 428
1536 CTTCCACATGAGC 1548
|:|:|:|:|:|
428 gTyrHisLeuSer 432

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